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GCTGCTCTGC TGCCCGGTGC TCAGCTCCGC GTACGCGCTG GTGGATGCAG ATGACGTCAT GACCAAAGAG GAGCAGATCT TCCTGCTGCA CCGCGCCCAG   400
 L  L  C   C  P  V  L   S  S  A   Y  A  L   V  D  A  D   D  V  M   T  K  E   E  Q  I  F   L  L  H   R  A  Q

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A  Q  C  Q   K  R  L   K  E  V   L  Q  R  P   A  D  I   M  E  S   D  K  G  W   A  S  A   S  T  S   G  K  P  K

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  K  E  K   A  S  G   K  L  Y  P   E  S  E   E  D  K   E  V  P  T   G  S  R   H  R  G   R  P  C  L   P  E  W

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 D  H  I   L  C  W  P   L  G  A   P  G  E   V  V  A  V   P  C  P   D  Y  I   Y  D  F  N   H  K  G   H  A  Y

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                                                                   I
GTGAACGGGA GGTGTTTGAC CGCCTGGGCA TGATCTACAC CGTGGGCTAC TCCGTGTCGC TGGCCTCCCT CACCGTGGCC GTGCTCATCC TGGCCTACTT   900
  E  R  E   V  F  D   R  L  G  M   I  Y  T   V  G  Y   S  V  S  L   A  S  L   T  V  A   V  L  I  L   A  Y  F
                                                                                   II
CAGGCGGCTG CACTGCACAC GCAACTACAT CCACATGCAC CTGTTCCTGT CCTTCATGCT TCGCGCCGTG AGCATCTTCG TCAAGGACGC GGTGCTCTAC   1000
 R  R  L   H  C  T  R   N  Y  I   H  M  H   L  F  L  S   F  M  L   R  A  V   S  I  F  V   K  D  A   V  L  Y

TCGGGCGCCA CGCTCGACGA GGCCGAGCGC CTCACGGAGG AAGAGCTGCG CGCCATCGCC CAGGCACCCC CGCCGCCCAC CGCCGCCGCC GGCTACGCGG   1100
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                                                                                         III
GCTGCAGGGT AGCTGTGACC TTCTTCCTTT ATTTCCTGGC CACCAACTAC TACTGGATTC TGGTGGAGGG GCTGTACCTG CATAGTCTCA TCTTCATGGC   1200
 C  R  V   A  V  T   F  F  L  Y   F  L  A   T  N  Y   Y  W  I  L   V  E  G   L  Y  L   H  S  L  I   F  M  A
                                                                   IV
CTTCTTCTCA GAGAAGAAGT ACCTGTGGGG CTTCACGGTC TTCGGCTGGG GTCTGCCCGC CGTCTTCGTG GCTGTGTGGG TCAGCGTGAG AGCCACCCTG   1300
 F  F  S   E  K  K  Y   L  W  G   F  T  V   F  G  W  G   L  P  A   V  F  V   A  V  W  V   S  V  R   A  T  L
                                                                                             V
GCCAACACCG GGTGCTGGGA CTTGAGCTCC GGGAACAAGA AGTGGATCAT CCAGGTGCCC ATCCTGGCCT CTATTGTGCT CAACTTCATC TTGTTCATCA   1400
A  N  T  G   C  W  D   L  S  S   G  N  K  K   W  I  I   Q  V  P   I  L  A  S   I  V  L   N  F  I   L  F  I  N

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  I  V  R   V  L  A   T  K  L  R   E  T  N   A  G  R   C  D  T  R   Q  Q  Y   R  K  L  L   K  S  T   L  V  L
    VI
CATGCCGCTC TTTGGCGTCC ACTACATCGT CTTCATGGCC ACGCCGTACA CCGAGGTCTC AGGGACGCTC TGGCAAGTCC AGATGCACTA CGAGATGCTC   1600
 M  P  L   F  G  V  H   Y  I  V   F  M  A   T  P  Y  T   E  V  S   G  T  L   W  Q  V  Q   M  H  Y   E  M  L
        VII
TTCAACTCCT TCCAGGGATT TTTTGTCGCC ATCATATACT GTTTCTGCAA TGGCGAGGTA CAGGCCGAGA TCAAGAAATC CTGGAGCCGC TGGACACTGG   1700
F  N  S  F   Q  G  F   F  V  A   I  I  Y  C   F  C  N   G  E  V   Q  A  E  I   K  K  S   W  S  R   W  T  L  A

CCCTGGACTT CAAGCGCAAG GCCCGAAGTG GGAGCAGCAG TTACAGCTAC GGCCCGATGG TGTCTCACAC GAGCGTGACC AACGTAGGCC CCCGCGCGGG   1800
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ACTTGGCCTG CCCCTCAGCC CCCGCCTGCT GCCCGCCGCT GCCGCCACCA CCACCGCCAC CACCAACGGC CACCCCCCGA TCCCGGGCCA CACCAAGCCA   1900
 L  G  L   P  L  S  P   R  L  L   P  A  A   A  A  T  T   T  A  T   T  N  G   H  P  P  I   P  G  H   T  K  P

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G  A  P  T   L  P  A   T  P  P   A  T  A  A   P  K  D   D  G  F   L  N  G  S   C  S  G   L  D  E   E  A  S  A

CGCCGGAGCG GCCTCCCGCC CTGCTGCAGG AGGAGTGGGA GACGGTCATG TGAtcgggga cctgtgccag ggttggactc gtggacataa gggccgacag   2100
  P  E  R   P  P  A   L  L  Q  E   E  W  E   T  V  M   .

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Fig. 1

SEQ ID NO: 1

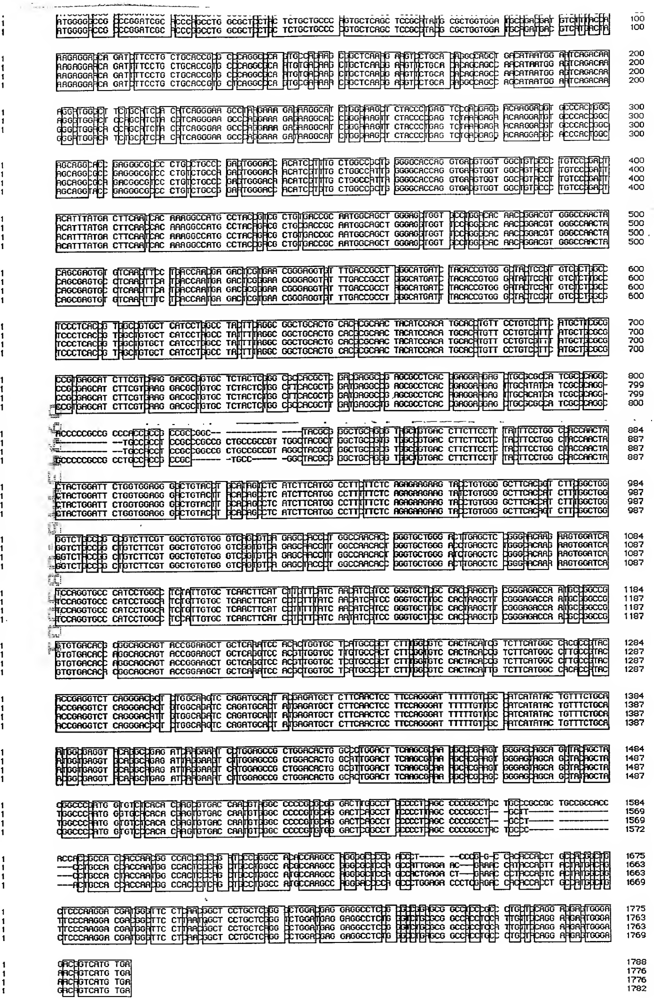

Fig. 2

SEQ ID NO: 2 (dPTH1)

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hPTH1      MGTARIAPGL ALLLCCPVLS SAYALVDADD VMTKEEQIFL LHRAQAQCEK RLKEVLQRPA SIMESDKGWT SASTSGKPRK DKASGKLYPE SEEDKEAPTG   1

dPTH1      SRHRGRPCLP EWDHILCWPL GAPGEVVAVP CPDYIYDFNH KGHAYRRCDR NGSWELVPGH NRTWANYSEC VKFLTNETRE REVFDRLGMI YTVGYSVSLA   2
rPTH1      SRRRGRPCLP EWDNIVCWPL GAPGEVVAVP CPDYIYDFNH KGHAYRRCDR NGSWEVVPGH NRTWANYSEC LKFMTNETRE REVFDRLGMI YTVGYSMSLA   2
mPTH1      SRRRGRPCLP EWDNIVCWPL GAPGEVVAVP CPDYIYDFNH KGHAYRRCDR NGSWEVVPGH NRTWANYSEC LKFMTNETRE REVFDRLGMI YTVGYSMSLA   2
hPTH1      SRYRGRPCLP EWDHILCWPL GAPGEVVAVP CPDYIYDFNH KGHAYRRCDR NGSWELVPGH NRTWANYSEC VKFLTNETRE REVFDRLGMI YTVGYSVSLA   2

dPTH1      SLTVAVLILA YFRRLHCTRN YIHMHLFLSF MLRAVSIFVK DAVLYSGATL DEAERLTEEE LRAIAQAPPP PTAAAGYAG CRVAVTFFLY FLATNYYWIL   2
rPTH1      SLTVAVLILA YFRRLHCTRN YIHMHMFLSF MLRAASIFVK DAVLYSGFTL DEAERLTEEE LHIIAQVPPP PAAAAVGYAG CRVAVTFFLY FLATNYYWIL   3
mPTH1      SLTVAVLILA YFRRLHCTRN YIHMHMFLSF MLRAASIFVK DAVLYSGFTL DEAERLTEEE LHIIAQVPPP PAAAAVGYAG CRVAVTFFLY FLATNYYWIL   3
hPTH1      SLTVAVLILA YFRRLHCTRN YIHMHLFLSF MLRAVSIFVK DAVLYSGATL DEAERLTEEE LRAIAQAPPP PATAAAGYAG CRVAVTFFLY FLATNYYWIL   3

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hPTH1      QQYRKLLKST LVLMPLFGVH YIVFMATPYT EVSGTLWQVQ MHYEMLFNSF QGFFVAIIYC FCNGEVQAEI KKSWSRWTLA LDFKRKARSG SSSYSYGPMV   5

dPTH1      SHTSVTNVGP RAGLGLPLSP RLLPAAATT TATTNGHPPI PGHTKPGAPT L---PATPPA TAAPKDDGFL NGSCSGLDEE ASAPERPPAL LQEEWETVM    5
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mPTH1      AHTSVTNVGP RAGLSLPLSP RLLPAT---- --T-NGHSQL PGHAKPGAPA IEN-ETIPVT MTVPKDDGFL NGSCSGLDEE ASGSARPPPL LQEEWETVM    5
hPTH1      SHTSVTNVGP RVGLGLPLSP RLLPTA---- --TTNGHPQL PGHAKPGTPA LETLETTPPA MAAPKDDGFL NGSCSGLDEE ASGPERPPAL LQEEWETVM    5
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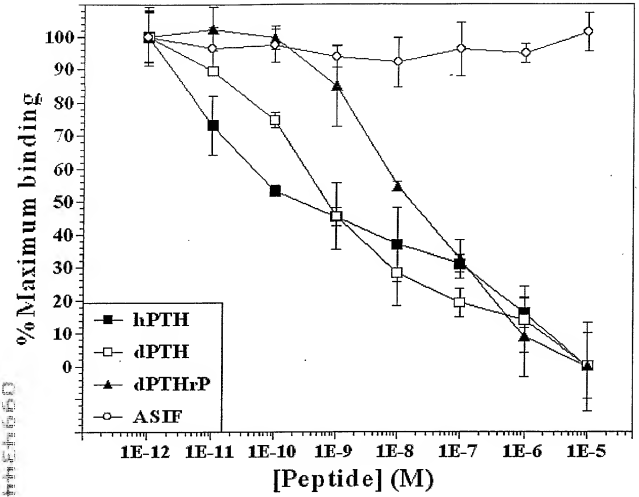
Fig. 3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dPTH
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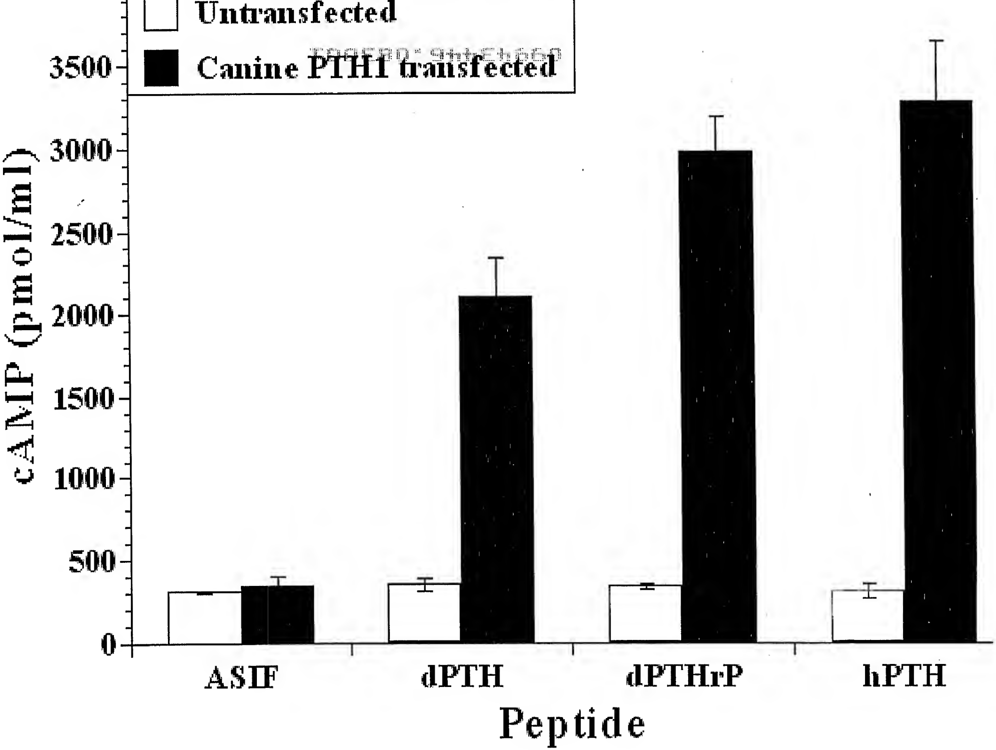
ASIF

Fig. 4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Peptide

Fig. 5